10/524,152

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=> d his

     (FILE 'HOME' ENTERED AT 16:17:08 ON 19 APR 2007)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 16:17:37 ON 19 APR 2007
L1            10 S GAMMA (W)PROTOBACTER?
L2             0 S CANDIDATUS (W)ENDOECETEIUNASCIDIA
L3          1838 S CANDIDATUS
L4         14868 S 16S (W)RIBOSOMAL(W)RNA
L5           114 S L3 AND L4
L6       8300433 S CLON? OR EXPRESS? OR RECOMBINANT
L7            33 S L5 AND L6
L8            26 DUP REM L7 (7 DUPLICATES REMOVED)
                 E ESTEBAN B P/AU
                 E PEREZ T A/AU
L9           621 S E2
                 E IGLESIAS A V/AU
                 E PELAEZ R H/AU
                 E MORENO R M/AU
L10           66 S E3-E6
L11          687 S L9 OR L10
L12            0 S L5 AND L11
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NEWS	2	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS	3	JAN 16	CA/CAplus Company Name Thesaurus enhanced and reloaded
NEWS	4	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS	5	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS	6	JAN 22	CA/CAplus updated with revised CAS roles
NEWS	7	JAN 22	CA/CAplus enhanced with patent applications from India
NEWS	8	JAN 29	PHAR reloaded with new search and display fields
NEWS	9	JAN 29	CAS Registry Number crossover limit increased to 300,000 in multiple databases
NEWS	10	FEB 15	PATDPASPC enhanced with Drug Approval numbers
NEWS	11	FEB 15	RUSSIAPAT enhanced with pre-1994 records
NEWS	12	FEB 23	KOREAPAT enhanced with IPC 8 features and functionality
NEWS	13	FEB 26	MEDLINE reloaded with enhancements
NEWS	14	FEB 26	EMBASE enhanced with Clinical Trial Number field
NEWS	15	FEB 26	TOXCENTER enhanced with reloaded MEDLINE
NEWS	16	FEB 26	IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS	17	FEB 26	CAS Registry Number crossover limit increased from 10,000 to 300,000 in multiple databases
NEWS	18	MAR 15	WPIDS/WPIX enhanced with new FRAGHITSTR display format
NEWS	19	MAR 16	CASREACT coverage extended
NEWS	20	MAR 20	MARPAT now updated daily
NEWS	21	MAR 22	LWPI reloaded
NEWS	22	MAR 30	RDISCLOSURE reloaded with enhancements
NEWS	23	MAR 30	INPADOCDB will replace INPADOC on STN
NEWS	24	APR 02	JICST-EPLUS removed from database clusters and STN

NEWS EXPRESS	NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS LOGIN	Welcome Banner and News Items
NEWS IPC8	For general information regarding STN implementation of IPC 8

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FILE 'HOME' ENTERED AT 16:17:08 ON 19 APR 2007

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=> file medline embase biosis biotechds scisearch hcaplus ntis lifesci
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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FILE 'LIFESCI' ENTERED AT 16:17:37 ON 19 APR 2007
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=> s gamma (w)protobacter?
L1          10 GAMMA (W) PROTOBACTER?

=> s candidatus (w)Endoeceteiunascidia
L2           0 CANDIDATUS (W) ENDOECETEIUNASCIDIA

=> s candidatus
L3        1838 CANDIDATUS

=> s 16s (w)ribosomal(w)RNA
L4       14868 16S (W) RIBOSOMAL(W) RNA

=> s l3 and l4
L5         114 L3 AND L4

=> s clon? or express? or recombinant
L6     8300433 CLON? OR EXPRESS? OR RECOMBINANT

=> s l5 and l6
L7          33 L5 AND L6

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8          26 DUP REM L7 (7 DUPLICATES REMOVED)

=> d 1-26 ibib ab

L8   ANSWER 1 OF 26     MEDLINE on STN                    DUPLICATE 1
ACCESSION NUMBER:    2007053312     IN-PROCESS
DOCUMENT NUMBER:     PubMed ID: 17215016
TITLE:               Quantification of anaerobic ammonium-oxidizing bacteria in
```

enrichment cultures by real-time PCR.
AUTHOR: Tsushima Ikuo; Kindaichi Tomonori; Okabe Satoshi
CORPORATE SOURCE: Department of Urban and Environmental Engineering, Graduate School of Engineering, Hokkaido University, North-13, West-8, Sapporo 060-8628, Japan.
SOURCE: Water research, (2007 Feb) Vol. 41, No. 4, pp. 785-94. Electronic Publication: 2007-01-09. Journal code: 0105072. ISSN: 0043-1354.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE: English
FILE SEGMENT: NONMEDLINE; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 30 Jan 2007 Last Updated on STN: 9 Mar 2007

AB The anaerobic ammonium-oxidizing (ANAMMOX) bacteria were enriched from a rotating disk reactor (RDR) biofilm in semi-batch cultures. Based on fluorescence in situ hybridization (FISH) analysis, this enrichment led to a relative population size of 36% ANAMMOX bacteria. Phylogenetic analysis revealed that all the detected clones were related to the previously reported ANAMMOX bacteria, Candidatus Brocadia anammoxidans (AF375994), with 92% sequence similarity. Furthermore, we successfully developed a real-time polymerase chain reaction (PCR) assay to quantify populations of ANAMMOX bacteria in the enrichment cultures. For this real-time PCR assay, PCR primer sets targeting 16S ribosomal RNA genes of ANAMMOX bacteria were designed and used. The quantification range of this assay was 6 orders of magnitude, from 8.9x10(1) to 8.9x10(6) copies per PCR, corresponding to the detection limit of 3.6x10(3) target copies mL(-1). A significant correlation was found between the increase in copy numbers of 16S rRNA gene of ANAMMOX bacteria and the increase in nitrogen removal rates in the enrichment cultures. Quantifying ANAMMOX bacterial populations in the enrichment culture made it possible to estimate the doubling time of the enriched ANAMMOX bacteria to be 3.6 to 5.4 days. The real-time PCR assay gave comparable population sizes in the enrichment cultures with the FISH results. These results suggest that the real-time PCR assay developed in this study is useful and reliable for quantifying the populations of ANAMMOX bacteria in environmental and engineering samples.

L8 ANSWER 2 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2007:65524 BIOSIS
DOCUMENT NUMBER: PREV200700061639
TITLE: 16S rRNA gene-based analysis of mucosa-associated bacterial community and phylogeny in the chicken gastrointestinal tracts: from crops to ceca.
AUTHOR(S): Gong, Jianhua [Reprint Author]; Si, Weiduo; Forster, Robert J.; Huang, Ruilin; Yu, Hai; Yin, Yulong; Yang, Chengbo; Han, Yanming
CORPORATE SOURCE: Agr and Agri Food Canada, Food Res Program, 93 Stone Rd W, Guelph, ON N1G 5C9, Canada
gongj@agr.gc.ca
SOURCE: FEMS Microbiology Ecology, (JAN 2007) Vol. 59, No. 1, pp. 147-157.
CODEN: FMECEZ. ISSN: 0168-6496.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 17 Jan 2007 Last Updated on STN: 17 Jan 2007

AB Mucosa-associated microbiota from different regions of the gastrointestinal (GI) tract of adult broilers was studied by analysis of 16S rRNA gene sequences. The microbiota mainly comprised Gram-positive bacteria along the GI tract. Fifty-one operational taxonomic units (OTUs) (from 98 clones) were detected in the ceca, as compared with 13 OTUs (from 49 clones) in the crops, 11 OTUs (from 51

clones) in the gizzard, 14 OTUs (from 52 clones) in the duodenum, 12 OTUs (from 50 clones) in the jejunum and nine OTUs (from 50 clones) in the ileum. Ceca were dominantly occupied by clostridia-related sequences (40%) with other abundant sequences being related to Faecalibacterium prausnitzii (14%), Escherichia coli (11%), lactobacilli (7%) and Ruminococcus (6%). Lactobacilli were predominant in the upper GI tract and had the highest diversity in the crop. Both Lactobacillus aviarius and Lactobacillus salivarius were the predominant species among lactobacilli. Candidatus division Arthromitus was also abundant in the jejunum and ileum.

L8 ANSWER 3 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2007:32729 BIOSIS
DOCUMENT NUMBER: PREV200700028308
TITLE: Devosia soli sp nov., isolated from greenhouse soil in Korea.
AUTHOR(S): Yoo, Seung-Hee; Weon, Hang-Yeon; Kim, Byung-Yong; Hong, Seung-Beom; Kwon, Soon-Wo [Reprint Author]; Cho, Yang-Hee; Go, Seung-Joo; Stackebrandt, Erko
CORPORATE SOURCE: Natl Agr Biotechnol, Rural Dev Adm, KACC, Genet Resources Div, Suwon 441707, South Korea
swkwon@rda.go.kr
SOURCE: International Journal of Systematic and Evolutionary Microbiology, (NOV 2006) Vol. 56, No. Part 11, pp. 2689-2692.
ISSN: 1466-5026.
DOCUMENT TYPE: Article
General Review; (Literature Review)
LANGUAGE: English
OTHER SOURCE: GenBank-U29386; EMBL-U29386; DDBJ-U29386; GenBank-DQ303125; EMBL-DQ303125; DDBJ-DQ303125; GenBank-D49423; EMBL-D49423; DDBJ-D49423; GenBank-AF469072; EMBL-AF469072; DDBJ-AF469072; GenBank-AJ86801; EMBL-AJ86801; DDBJ-AJ86801; GenBank-AJ548825; EMBL-AJ548825; DDBJ-AJ548825
ENTRY DATE: Entered STN: 27 Dec 2006
Last Updated on STN: 27 Dec 2006
AB A Gram-negative, obligately aerobic, rod-shaped bacterium was isolated from greenhouse soil used to cultivate lettuce. The strain, GH2-10(T), was characterized on the basis of phenotypic and genotypic data. 16S rRNA gene sequence analysis revealed that the isolate belonged to the genus Devosia, with highest sequence similarity (98.5%) to Devosia riboflavina IFO 13584(T). Sequence similarities with other strains tested were below 97.0%. Strain GH2-10(T) had Q-10 as the predominant ubiquinone and C(18:1)w7c and C-16:0 as the major fatty acids. The G + C content of the genomic DNA was 59.5 mol%. The results of DNA-DNA hybridization experiments (47% relatedness between D. riboflavina DSM 7230(T) and strain GH2-10(T)) and physiological and biochemical tests suggested that strain GH2-10(T) represents a novel species of the genus Devosia, for which the name Devosia soli sp. nov. is proposed. The type strain is GH2-10(T) (= KACC 11509(T) =DSM 17780(T)).

L8 ANSWER 4 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2007:32703 BIOSIS
DOCUMENT NUMBER: PREV200700028282
TITLE: 'Candidatus Midichloria mitochondrii', an endosymbiont of the tick Ixodes ricinus with a unique intramitochondrial lifestyle.
AUTHOR(S): Sassera, Davide; Beninati, Tiziana; Bandi, Claudio; Bouman, Edwin A. P.; Sacchi, Luciano; Fabbi, Massimo; Lo, Nathan [Reprint Author]
CORPORATE SOURCE: Univ Sydney, Sch Biol Sci, Sydney, NSW 2006, Australia
nathan@usyd.edu.au
SOURCE: International Journal of Systematic and Evolutionary Microbiology, (NOV 2006) Vol. 56, No. Part 11, pp.

2535-2540.
ISSN: 1466-5026.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Dec 2006
Last Updated on STN: 27 Dec 2006

AB An intracellular bacterium with the unique ability to enter mitochondria exists in the European vector of Lyme disease, the hard tick Ixodes ricinus. Previous phylogenetic analyses based on 16S rRNA gene sequences suggested that the bacterium formed a divergent lineage within the Rickettsiales (Alphaproteobacteria). Here, we present additional phylogenetic evidence, based on the gyrB gene sequence, that confirms the phylogenetic position of the bacterium, Based on these data, as well as electron microscopy (EM), in situ hybridization and other observations, we propose the name 'Candidatus Miclichloria mitochondrii' for this bacterium. The symbiont appears to be ubiquitous in females of L ricinus across the tick's distribution, while lower prevalence is observed in males (44%). Based on EM and in situ hybridization studies, the presence of 'Candidatus M. mitochondrii' in females appears to be restricted to ovarian cells. The bacterium was found to be localized both in the cytoplasm and in the intermembrane space of the mitochondria of ovarian cells. 'Candidatus M. mitochondrii' is the first bacterium to be identified that resides within animal mitochondria.

L8 ANSWER 5 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
DUPLICATE 2
ACCESSION NUMBER: 2006:530980 BIOSIS
DOCUMENT NUMBER: PREV200600529805
TITLE: Simplified DNA extraction and improved PCR based detection of greening bacterium in citrus.
AUTHOR(S): Gouda, K. A.; Baranwal, V. K. [Reprint Author]; Ahlawat, Y. S.
CORPORATE SOURCE: Indian Agr Res Inst, Virol Unit, Div Plant Pathol, New Delhi 110012, India
vbaranwal2001@yahoo.com
SOURCE: Journal of Plant Biochemistry and Biotechnology, (JUL 2006) Vol. 15, No. 2, pp. 117-121.
ISSN: 0971-7811.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 12 Oct 2006
Last Updated on STN: 12 Oct 2006

AB Citrus greening disease caused by a fastidious bacterium is an important graft transmissible disease in commercial citrus in India and other parts of the world. Polymerase chain reaction (PCR) is a sensitive and convenient method for detection of greening bacterium. A non-phenol chloroform method of DNA extraction was evaluated for DNA quality and PCR based detection of greening bacterium. The method was comparable with a commercial DNA extraction kit (Qlagen) and better than a CTAB based DNA extraction method. To improve the reliability, three primer sets (primers A, B, and C yielding amplicons of 1160 bp, 703 bp and 451 bp, respectively) and two polymerase enzymes (Taq polymerase and Klan Taq polymerase) were evaluated. The primer set C provided better amplification when compared to primer sets A and B. Primer C in combination with Taq polymerase provided amplification band at a DNA template concentration of 100 pg but good amplification band was obtained at still lower DNA template concentration of 0.1 pg when Klen Taq polymerase was used. The standardized PCR protocol combining non-phenol chloroform method of DNA isolation, primer set C and Klen Taq polymerase enzyme was found very effective in detecting greening bacterium in citrus trees. The sequence of cloned amplicon from 16S ribosomal RNA gene had 89 - 100 % sequence identity with corresponding sequence of Candidatus Liheribacter asiaticus from China, Brazil, Japan and Pune isolate of India, C. Liberibacter americnus

from Brazil and C. Liberibacter africanus from Africa.

L8 ANSWER 6 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2007:32872 BIOSIS
DOCUMENT NUMBER: PREV200700028334
TITLE: Detection of phytoplasma in insects collected in witches' broom affected lime groves.
AUTHOR(S): Siampour, M.; Izadpanah, K. [Reprint Author]; Afsharifar, A. R.; Salehi, M.; Taghizadeh, M.
CORPORATE SOURCE: Shiraz Univ, Dept Plant Protect, Coll Agr, Shiraz, Iran
SOURCE: Iranian Journal of Plant Pathology, (2006) Vol. 42, No. 1, pp. 35-38.
ISSN: 0006-2774.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Dec 2006
Last Updated on STN: 27 Dec 2006

AB Despite severe damage of witches' broom disease of lime (WBDL) and its apparent natural spread in affected groves, vector of its associated phytoplasma has remained undetermined. The aim of the present investigation was to study various insects for their possible involvement in transmission of this phytoplasma. Piercing-sucking insects were collected by sweep net in infected lime groves in different seasons in 2003 and 2004. Samplings were carried out in affected lime groves in Hormozgan and Kerman Provinces. Nested PCR followed by RFLP or cloning and sequencing were used for detection and identification of phytoplasmas in insect bodies.Results of this study revealed that the 16s rRNA gene of WBDL phytoplasma is detectable in leafhopper species Hishimonus phycitis, Recilia schmidtgeni and Idioscopus clypealis and in citrus psylla, Diaphorina citri. Further studies indicated that Candidatus Phytoplasma aurantifolia persists in the body of H. phycitis and D. citri for several weeks after feeding on healthy lime seedlings. Partial sequence of a phytoplasmal 16s rRNA gene similar to that of WBDL phytoplasma. was detectable in the head and salivary glands and in the sucrose solution used as feeding medium for Hishimonus phycitis. H. phycitis and D. citri were the only piercing-sucking insects collected on lime trees.

L8 ANSWER 7 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2005:363752 BIOSIS
DOCUMENT NUMBER: PREV200510144697
TITLE: Microbial diversity in ultra-high-pressure rocks and fluids from the Chinese Continental Scientific Drilling Project in China.
AUTHOR(S): Zhang, Gengxin; Dong, Hailiang [Reprint Author]; Xu, Zhiqin; Zhao, Donggao; Zhang, Chuanlun
CORPORATE SOURCE: Miami Univ, Dept Geol, Oxford, OH 45056 USA
dongh@muohio.edu
SOURCE: Applied and Environmental Microbiology, (JUN 2005) Vol. 71, No. 6, pp. 3213-3227.
CODEN: AEMIDF. ISSN: 0099-2240.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 14 Sep 2005
Last Updated on STN: 14 Sep 2005

AB Microbial communities in ultra-high-pressure (UHP) rocks and drilling fluids from the Chinese Continental Scientific Drilling Project were characterized. The rocks had a porosity of I to 3.5% and a permeability of similar to 0.5 mDarcy. Abundant fluid and gas inclusions were present in the minerals. The rocks contained significant amounts of Fe2O3, FeO, P2O5, and nitrate (3 to 16 ppm). Acridine orange direct counting and phospholipid fatty acid analysis indicated that the total counts in the rocks and the fluids were 5.2 X 10(3) to 2.4 X 10(4) Cells/g and 3.5 X 10(8) to 4.2 X 10(9) cells/g, respectively. Enrichment assays resulted in

successful growth of thermophilic and alkaliphilic bacteria from the fluids, and some of these bacteria reduced Fe(111) to magnetite. 16S rRNA gene analyses indicated that the rocks were dominated by sequences similar to sequences of Proteobacteria and that most organisms were related to nitrate reducers from a saline, alkaline, cold habitat; however, some phylotypes were either members of a novel lineage or closely related to uncultured clones. The bacterial communities in the fluids were more diverse and included Proteobacteria, Bacteroidetes, gram-positive bacteria, Planctomycetes, and Candidatus taxa. The archaeal diversity was lower, and most sequences were not related to any known cultivated species. Some archaeal sequences were 90 to 95% similar to sequences recovered from ocean sediments or other subsurface environments. Some archaeal sequences from the drilling fluids were > 93% similar to sequences of Sulfolobus solfataricus., and the thermophilic nature was consistent with the in situ temperature. We inferred that the microbes in the UHP rocks reside in fluid and gas inclusions, whereas those in the drilling fluids may be derived from subsurface fluids.

L8 ANSWER 8 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2006:18805 BIOSIS
DOCUMENT NUMBER: PREV200600021470
TITLE: 'Candidatus Liberibacter americanus', associated with citrus huanglongbing (greening disease) in Sao Paulo State, Brazil.
AUTHOR(S): do Carmo Teixeira, Diva; Saillard, Colette; Eveillard, Sandrine [Reprint Author]; Danet, Jean Luc; da Costa, Paulo Inacio; Ayres, Antonio Juliano; Bove, Joseph
CORPORATE SOURCE: INRA, UMR 1090, BP 81, F-33883 Villenave Dornon, France jagoueix@bordeaux.inra.fr
SOURCE: International Journal of Systematic and Evolutionary Microbiology, (SEP 2005) Vol. 55, No. Part 5, pp. 1857-1862.
ISSN: 1466-5026.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 21 Dec 2005
Last Updated on STN: 21 Dec 2005

AB Symptoms of huanglongbing (HLB) were reported in Sao Paulo State (SPS), Brazil, in March 2004. In Asia, HLB is caused by 'Candidatus Liberibacterasiaticus'and in Africa by 'Candidatus Liberibacter africanus'. Detection of the liberibacters is based on PCR amplification of their 16S rRNA gene with specific primers. Leaves with blotchy mottle symptoms characteristic of HLB were sampled in several farms of SIPS and tested for the presence of liberibacters. 'Ca. L. asiaticus' was detected in a small number of samples but most samples gave negative PCR results. Therefore, a new HLB pathogen was suspected. Evidence for an SPS-HLB bacterium in symptomatic leaves was obtained by PCR amplification with universal primers for prokaryotic 16S rRNA gene sequences. The amplified 16S rRNA gene was cloned and sequenced. Sequence analysis and phylogeny studies showed that the 16S rRNA gene possessed the oligonucleotide signatures and the secondary loop structure characteristic of the alpha-Proteobacteria, including the liberibacters. The 16S rRNA gene sequence phylogenetic tree showed that the SPS-HLB bacterium clustered within the a-Proteobacteria, the liberibacters being its closest relatives. For these reasons, the SPS-HLB bacterium is considered a member of the genus 'Ca. Liberibacter'. However, while the 16S rRNA gene sequences of 'Ca. L. asiaticus' and 'Ca. L. africanus' had 98-4% similarity, the 16S rRNA gene sequence of the SPS-HLB liberibacter had only 96(.)0% similarity with the 16S rRNA gene sequences of 'Ca. L. asiaticus'or'Ca. L. africanus'. This lower similarity was reflected in the phylogenetic tree, where the SPS-HLB liberibacter did not cluster within the 'Ca. L asiaticus'/'Ca. L. africanus group', but as a separate branch. Within the genus 'Candidatus Liberibacter' and for a given species, the 16S/23S intergenic region does not vary greatly. The

intergenic regions of three strains of 'Ca. L. asiaticus', from India, the People's Republic of China and Japan, were found to have identical or almost identical sequences. In contrast, the intergenic regions of the SPS-HLB liberibacter, 'Ca. L. asiaticus' and 'Ca. L. africanus' had quite different sequences, with similarity between 66(.)0 and 79(.)5%. These results confirm that the SPS-HLB liberibacter is a novel species for which the name 'Candidatus Liberibacter americanus' is proposed. Like the African and the Asian liberibacters, the 'American' liberibacter is restricted to the sieve tubes of the citrus host. The liberibacter could also be detected by PCR amplification of the 16S rRNA gene in Diaphorina citri, the psyllid vector of 'Ca. L. asiaticus', suggesting that this psyllid is also a vector of 'Ca. L. americanus' in SPS. 'Ca. L. americanus' was detected in 216 of 218 symptomatic leaf samples from 47 farms in 35 municipalities, while 'Ca. L. asiaticus' was detected in only 4 of the 218 samples, indicating that 'Ca. L. americanus' is the major cause of HLB in SIPS.

L8 ANSWER 9 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:894781 SCISEARCH
THE GENUINE ARTICLE: 860PT
TITLE: "Candidatus Hepatoplasma crinochetorum," a new, stalk-forming lineage of Mollicutes colonizing the midgut glands of a terrestrial isopod
AUTHOR: Wang Y J (Reprint); Stingl U; Anton-Erxleben F; Geisler S; Brune A; Zimmer M
CORPORATE SOURCE: Univ Kiel, Inst Zool, Olshaussenstr 40, D-24098 Kiel, Germany (Reprint); Univ Kiel, Inst Zool, D-24098 Kiel, Germany; Univ Konstanz, Fachbereich Biol, LS Mikrobielle Okol, D-7750 Constance, Germany; Max Planck Inst Terr Mikrobiol, Marburg, Germany
ywang@zoologie.uni-kiel.de
COUNTRY OF AUTHOR: Germany
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (OCT 2004) Vol. 70, No. 10, pp. 6166-6172.
ISSN: 0099-2240.
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 32
ENTRY DATE: Entered STN: 5 Nov 2004
Last Updated on STN: 5 Nov 2004

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Uncultivated bacteria that densely colonize the midgut glands (hepatopancreas) of the terrestrial isopod Porcellio scaber (Crustacea:Isopoda) were identified by cloning and sequencing of their 16S rRNA genes. Phylogenetic analysis revealed that these symbionts represent a novel lineage of the Mollicutes and are only distantly related (<82% sequence identity) to members of the Mycoplasmatales and Entomoplasmatales. Fluorescence in situ hybridization with a specific oligonucleotide probe confirmed that the amplified 16S rRNA gene sequences indeed originated from a homogeneous population of symbionts intimately associated with the epithelial surface of the hepatopancreas. The same probe also detected morphotypically identical symbionts in other crinochete isopods. Scanning and transmission electron microscopy revealed uniform spherical bacterial cells without a cell wall, sometimes interacting with the microvilli of the brush border by means of stalk-like cytoplasmic appendages, which also appeared to be involved in cell division through budding. Based on the isolated phylogenetic position and unique cytological properties, the provisional name "Candidatus Hepatoplasma crinochetorum" is proposed for this new taxon of Mollicutes colonizing the hepatopancreas of P. scaber.

L8 ANSWER 10 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:684575 SCISEARCH
THE GENUINE ARTICLE: 840KQ
TITLE: Symbionts of the gut flagellate Stauroojoenina sp from Neotermes cubanus represent a novel, termite-associated lineage of Bacteroidales: description of 'Candidatus Vestibaculum illigatum'
AUTHOR: Stingl U; Maass A; Radek R; Brune A (Reprint)
CORPORATE SOURCE: Univ Konstanz, Fachbereich Biol, LS Mikrobielle Okol, D-78457 Constance, Germany (Reprint); Free Univ Berlin, AG Protozool, Inst Biol Zool, D-14195 Berlin, Germany; Max Planck Inst Terr Microbiol, D-35043 Marburg, Germany brune@staff.uni-marburg.de
COUNTRY OF AUTHOR: Germany
SOURCE: MICROBIOLOGY-SGM, (JUL 2004) Vol. 150, Part 7, pp. 2229-2235.
ISSN: 1350-0872.
PUBLISHER: SOC GENERAL MICROBIOLOGY, MARLBOROUGH HOUSE, BASINGSTOKE RD, SPENCERS WOODS, READING RG7 1AG, BERKS, ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 46
ENTRY DATE: Entered STN: 20 Aug 2004
Last Updated on STN: 20 Aug 2004

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The symbioses between cellulose-degrading flagellates and bacteria are one of the most fascinating phenomena in the complex micro-ecosystem found in the hindgut of lower termites. However, little is known about the identity of the symbionts. One example is the epibiotic bacteria colonizing the surface of hypermastigote protists of the genus Staurojoenina. By using scanning electron microscopy, it was shown that the whole surface of Staurojoenina sp. from the termite Neotermes cubanus is densely covered with long rod-shaped bacteria of uniform size and morphology. PCR amplification of 16S rRNA genes from isolated protozoa and subsequent cloning yielded a uniform collection of clones with virtually identical sequences. Phylogenetic analysis placed them as a new lineage among the Bacteroidales, only distantly related to other uncultivated bacteria in the hindgut of other termites, including an epibiont of the flagellate Mixotricha paradoxa. The closest cultivated relative was Tannerella forsythensis (<85% sequence identity). Fluorescence in situ hybridization with a newly designed clone -specific oligonucleotide probe confirmed that these sequences belong to the rod-shaped epibionts of Staurojoenina sp. Transmission electron microscopy confirmed the presence of a Gram-negative cell wall and revealed special attachment sites for the symbionts on the cell envelope of the flagellate host. Based on the isolated phylogenetic position and the specific association with the surface of Staurojoenina sp., we propose to classify this new taxon of Bacteroidales under the provisional name 'Candidatus Vestibaculum illigatum'.

L8 ANSWER 11 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:741762 SCISEARCH
THE GENUINE ARTICLE: 844IO
TITLE: 'Candidcatus Phytoplasma', a taxon for the wall-less, non-helical prokaryotes that colonize plant phloem and insects
AUTHOR: Firrao G (Reprint); Andersen M; Bertaccini A; Boudon E; Bove J M; Daire X; Davis R E; Fletcher J; Garnier M; Gibb K S; Gundersen-Rindal D E; Harrison N; Hiruki C; Kirkpatrick B C; Jones P; Kuske C R; Lee I M; Liefting L; Marcone C; Namba S; Schneider B; Sears B B; Seemuller E; Smart C D; Streten C; Wang K

CORPORATE SOURCE: Univ Udine, I-33100 Udine, Italy (Reprint); HortRes, Auckland, New Zealand; Alma Mater Studiorum Univ Bologna, Bologna, Italy; INRA, F-21034 Dijon, France; Univ Bordeaux 2, F-33076 Bordeaux, France; INRA, IBVM, Villenave Dornon, France; USDA ARS, Beltsville, MD USA; Oklahoma State Univ, Stillwater, OK 74078 USA; INRA, Villenave Dornon, France; Charles Darwin Univ, Darwin, NT, Australia; Univ Florida, Ft Lauderdale, FL USA; Univ Alberta, Edmonton, AB, Canada; Univ Calif Davis, Davis, CA 95616 USA; Rothamsted Res, Harpenden, Herts, England; Los Alamos Natl Lab, Los Alamos, NM USA; Univ Basilicata, I-85100 Potenza, Italy; Univ Tokyo, Tokyo, Japan; Biol Bundesanstalt, Dossenheim, Germany; Michigan State Univ, E Lansing, MI 48824 USA; Cornell Univ, Geneva, NY USA
Corporate Author: IRPCM Phytoplasma Spiroplasma Work
firrao@uniud.it
COUNTRY OF AUTHOR: Italy; New Zealand; France; USA; Australia; Canada; England; Japan; Germany
SOURCE: INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY, (JUL 2004) Vol. 54, Part 4, pp. 1243-1255. ISSN: 1466-5026.
PUBLISHER: SOC GENERAL MICROBIOLOGY, MARLBOROUGH HOUSE, BASINGSTOKE RD, SPENCERS WOODS, READING RG7 1AG, BERKS, ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 96
ENTRY DATE: Entered STN: 10 Sep 2004
Last Updated on STN: 10 Sep 2004
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The trivial name 'phytoplasma' has been adopted to collectively name wall-less, non-helical prokaryotes that colonize plant phloem and insects, which were formerly known as mycoplasma-like organisms. Although phytoplasmas have not yet been cultivated in vitro, phylogenetic analyses based on various conserved genes have shown that they represent a distinct, monophyletic clade within the class Mollicutes. It is proposed here to accommodate phytoplasmas within the novel genus 'Candidatus (Ca.) Phytoplasma'. Given the diversity within 'Ca. Phytoplasma', several subtaxa are needed to accommodate organisms that share < 97-5% similarity among their 16S rRNA gene sequences. This report describes the properties of 'Ca. Phytoplasma', a taxon that includes the species 'Ca. Phytoplasma aurantifolia' (the prokaryote associated with witches'-broom disease of small-fruited acid lime), 'Ca. Phytoplasma australiense' (associated with Australian grapevine yellows), 'Ca. Phytoplasma fraxini' (associated with ash yellows), 'Ca. Phytoplasma japonicum' (associated with Japanese hydrangea phyllody), 'Ca. Phytoplasma brasiliense' (associated with hibiscus witches'-broom in Brazil), 'Ca. Phytoplasma castaneae' (associated with chestnut witches'-broom in Korea), 'Ca. Phytoplasma asteris' (associated with aster yellows), 'Ca. Phytoplasma mali' (associated with apple proliferation), 'Ca. Phytoplasma phoenicium' (associated with almond lethal disease), 'Ca. Phytoplasma trifolii' (associated with clover proliferation), 'Ca. Phytoplasma cynodontis' (associated with Bermuda grass white leaf), 'Ca. Phytoplasma ziziphi' (associated with jujube witches'-broom), 'Ca. Phytoplasma oryzae' (associated with rice yellow dwarf) and six species-level taxa for which the Candidatus species designation has not yet been formally proposed (for the phytoplasmas associated with X-disease of peach, grapevine flavescence doree, Central American coconut lethal yellows, Tanzanian lethal decline of coconut, Nigerian lethal decline of coconut and loofah witches'-broom, respectively). Additional species are needed to accommodate organisms that, despite their 16S rRNA gene sequence being >97.5% similar to those of other 'Ca. Phytoplasma' species, are characterized by distinctive biological, phytopathological and genetic properties. These include 'Ca. Phytoplasma pyri' (associated with pear decline), 'Ca. Phytoplasma

prunorum' (associated with European stone fruit yellows), 'Ca. Phytoplasma spartii' (associated with spartium witches'-broom), 'Ca. Phytoplasma rhamni' (associated with buckthorn witches'-broom), 'Ca. Phytoplasma allocasuarinae' (associated with allocasuarina yellows), 'Ca. Phytoplasma ulmi' (associated with elm yellows) and an additional taxon for the stolbur phytoplasma. Conversely, some organisms, despite their 16S rRNA gene sequence being < 97-5% similar to that of any other 'Ca. Phytoplasma' species, are not presently described as Candidatus species, due to their poor overall characterization.

L8 ANSWER 12 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:989113 SCISEARCH
THE GENUINE ARTICLE: 864XF
TITLE: "Candidatus phytoplasma australiense" in Coprosma robusta in New Zealand
AUTHOR: Beever R E (Reprint); Wood G A; Andersen M T; Pennycook S R; Sutherland P W; Forster R L S
CORPORATE SOURCE: Landcare Res, Private Bag 92170, Auckland, New Zealand (Reprint); Landcare Res, Auckland, New Zealand; Hort & Food Res Inst New Zealand Ltd, Auckland, New Zealand; Agrigenesis Biosci Ltd, Auckland, New Zealand
COUNTRY OF AUTHOR: New Zealand
SOURCE: NEW ZEALAND JOURNAL OF BOTANY, (SEP 2004) Vol. 42, No. 4, pp. 663-675.
ISSN: 0028-825X.
PUBLISHER: SIR PUBLISHING, PO BOX 399, WELLINGTON, NEW ZEALAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 42
ENTRY DATE: Entered STN: 2 Dec 2004
Last Updated on STN: 2 Dec 2004

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A phytoplasma is reported from wild plants of Coprosma robusta, where it is associated with leaf reddening or bronzing and dieback of shoots and branches. It was detected by electron microscopy of phloem tissue, and by one-step and nested PCR using phytoplasma-specific primers targeting the 16S rRNA gene. The sequence of the 16S product closely matches that of the Phormium yellow leaf phytoplasma and places the phytoplasma in the putative species "Candidatus Phytoplasma australiense". It was transmitted by grafting to C. robusta and C. macrocarpa. The symptoms of the disease caused by the phytoplasma (Coprosma lethal decline) in clonally matched graft-inoculated versus ungrafted cuttings of C. robusta included interveinal chlorosis and abnormal leaf yellowing or reddening, slowing of growth, and shoot dieback. A field survey of C. robusta indicated that shoot dieback and abnormal leaf coloration are common throughout much of New Zealand. "Ca. P. australiense" was detected in some, but not all, symptomatic plants, indicating it may play a role in causing such symptoms in the field. It is proposed that infected C. robusta plants provide a reservoir of "Ca. P. australiense" that leads to infection of other hosts.

L8 ANSWER 13 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2005:111722 SCISEARCH
THE GENUINE ARTICLE: 889SN
TITLE: Molecular investigation of the microbial populations of the pink sugarcane mealybug, Saccharicoccus sacchari
AUTHOR: Franke-Whittle I H (Reprint); O'Shea M G; Leonard G J; Sly L I
CORPORATE SOURCE: Univ Queensland, Ctr Bacterial Divers & Identificat, Dept Microbiol & Parasitol, Brisbane, Qld 4072, Australia (Reprint); BSES Ltd, David N Plant Res Ctr, Brisbane, Qld 4068, Australia

ingrid.whittle@uibk.ac.at
COUNTRY OF AUTHOR: Australia
SOURCE: ANNALS OF MICROBIOLOGY, (2004) Vol. 54, No. 4, pp. 455-470

ISSN: 1590-4261.
PUBLISHER: INST MICROBIOLOGIA, VIA CELORIA 2, 20133 MILAN, ITALY.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 52
ENTRY DATE: Entered STN: 10 Feb 2005
Last Updated on STN: 10 Feb 2005
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In an attempt to better understand the microbial diversity and endosymbiotic microbiota of the pink sugarcane mealybug (PSMB) Saccharicoccus sacchari Cockerell (Homoptera: Pseudococcidae), culture-independent approaches, namely PCR, a 16S rDNA clone library, and temperature gradient gel electrophoresis (TGGE) were used. Previous work has indicated that the acetic acid bacteria Gluconacetobacter sacchari, Gluconacetobacter diazotrophicus, and Gluconacetobacter liquefaciens represent only a small proportion of the microbial community of the PSMB. These findings were supported in this study by TGGE, where no bands representing G. sacchari, G. diazotrophicus, and G. liquefaciens on the acrylamide gel could be observed following electrophoresis, and by a 16S rDNA clone library study, where no clones with the sequence of an acetic acid bacterium were found. Instead, TGGE revealed that the mealybug microbial community was dominated by beta- and gamma-Proteobacteria. The dominant band in TGGE gels found in a majority of the mealybug samples was most similar, according to BLAST analysis, to the beta-symbiont of the craw mealybug Antonina crawii and to "Candidatus" Tremblaya princeps, an endosymbiont from the mealybug Paracoccus nothofagicola. The sequences of other dominant bands were identified as gamma-Proteobacteria, and were most closely related to uncultured bacterial clones obtained from soil samples. Mealybugs collected from different areas in Queensland, Australia, were found to produce similar TGGE profiles, although there were a few exceptions. A 16S rDNA clone library based on DNA extracted from a mealybug collected from sugarcane in the Burdekin region in Queensland, Australia, indicated very low levels of diversity among mealybug microbial populations. All sequenced clones were most closely related to the same members of the gamma-Proteobacteria, according to BLAST analysis.

L8 ANSWER 14 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2005:112121 BIOSIS
DOCUMENT NUMBER: PREV200500114137
TITLE: The high prevalence of Helicobacter sp. in porcine pyloric mucosa and its histopathological and molecular characteristics.
AUTHOR(S): Park, Jong-Hwan; Seok, Seung-Hyeok; Cho, Sun-A; Baek, Min-Won; Lee, Hui-Young; Kim, Dong-Jae; Park, Jae-Hak [Reprint Author]
CORPORATE SOURCE: Coll Vet MedSch Agr BiotechnolDept Lab Anim Med, Seoul Natl Univ, San 56-1,Sillim Dong, Seoul, 151742, South Korea pjhak@snu.ac.kr
SOURCE: Veterinary Microbiology, (December 9 2004) Vol. 104, No. 3-4, pp. 219-225. print.
CODEN: VMICDQ. ISSN: 0378-1135.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 23 Mar 2005
Last Updated on STN: 23 Mar 2005

AB This study examined the prevalence of Helicobacter infection in the pyloric mucosa of pigs and its histopathological and molecular

characteristics. Forty porcine pyloric samples were examined for Helicobacter infection by silver staining and PCR assay. The PCR product (376 bp) was digested with NdeII to differentiate between Helicobacter heilmannii and Helicobacter pylori. Another PCR assay run to produce an 1157 bp fragment was performed using a primer set designed from the 16S rRNA gene of Candidatus H. suis, and its product was cloned and sequenced. Infection rates were 62.5% (25/40) and 95.0% (38/40) as determined by silver staining and the PCR assay, respectively. On histopathological examination, lymphoid follicle aggregation in the pyloric mucosa and granulocytic migration into the lumen of pyloric glands were observed in 24 (60.0%) and 33 (82.5%) gastric samples, respectively. All PCR products, except that of H. pylori, were cut into two fragments of 147 and 229 bp by enzymatic digestion with NdeII. Sequencing of the 16S rRNA gene showed that the bacterium had 99.57% (1152 bp/1157 bp) homology to the 16S rRNA gene of Candidatus H. suis.

L8 ANSWER 15 OF 26 SCISEARCH

ACCESSION NUMBER: 2003:493553 SCISEARCH
THE GENUINE ARTICLE: 685XE
TITLE: Microbial composition and structure of a rotating biological contactor biofilm treating ammonium-rich wastewater without organic carbon
AUTHOR: Egli K; Bosshard F; Werlen C; Lais P; Siegrist H; Zehnder A J B; van der Meer J R (Reprint)
CORPORATE SOURCE: Swiss Fed Inst Environm Sci & Technol, CH-8600 Dubendorf, Switzerland (Reprint); Sondermulldeponie Kolliken, CH-5742 Kolliken, Switzerland
COUNTRY OF AUTHOR: Switzerland
SOURCE: MICROBIAL ECOLOGY, (MAY 2003) Vol. 45, No. 4, pp. 419-432. ISSN: 0095-3628.
PUBLISHER: SPRINGER-VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010 USA.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 48
ENTRY DATE: Entered STN: 27 Jun 2003
Last Updated on STN: 27 Jun 2003
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB High nitrogen losses were observed in a rotating biological contactor (RBV) treating ammonium-rich (up to 500 mg NH4+-N/L) but organic-carbon-poor leachate from a hazardous waste landfill in Kollliken, Switzerland. The composition and spatial structure of the microbial community in the biofilm on the RBC was analyzed with specific attention for the presence of aerobic ammonium and nitrite oxidizing bacteria and anaerobic ammonium oxidizers. Anaerobic ammonium oxidation (anammox) involves the oxidation of ammonium with nitrite to N-2. First the diversity of the biofilm community was determined from sequencing cloned PCR-amplified 16S rDNA fragments. This revealed the presence of a number of very unusual 16S rDNA sequences, but very few sequences related to known ammonium or nitrite oxidizing bacteria. From analysis of biofilm samples by fluorescence in situ hybridization with known phylogenetic probes and by dot-blot hybridization of the same probes to total RNA purified from biofilm samples, the main groups of microorganisms constituting the biofilm. were found to be ammonium-oxidizing bacteria from the Nitrosomonas europaea/eutropha group, anaerobic ammonium-oxidizing bacteria of the "Candidatus Kuenenia stuttgartiensis" type, filamentous bacteria from the phylum, Bacteroidetes, and nitrite-oxidizing bacteria from the genus Nitrospira. Aerobic and anaerobic ammonium-oxidizing bacteria were present in similar amounts of around 20 to 30% of the biomass, whereas members of the CFB phylum were present at around 7%. Nitrite oxidizing bacteria were only present in relatively low amounts (less than 5% determined with

fluorescence in situ hybridization). Data from 16S rRNA dot-blot and in situ hybridization were not in all cases congruent. FISH analysis of thin-sliced and fixed biofilm samples clearly showed that the aerobic nitrifiers were located at the top of the biofilm in an extremely high density and in alternating clusters. Anammox bacteria were exclusively present in the lower half of the biofilm, whereas CFB-type filamentous bacteria were present throughout the biofilm. The structure and composition of these biofilms correlated very nicely with the proposed physiological functional separations in ammonium conversion.

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ACCESSION NUMBER: 2004:11023 BIOSIS
DOCUMENT NUMBER: PREV200400014896
TITLE: Differential amplification of sequence heterogeneous ribosomal RNA genes and classification of the 'Fragaria multicipita' phytoplasma.
AUTHOR(S): Davis, Robert E. [Reprint Author]; Jomantiene, Rasa; Kalvelyte, Audrone; Dally, Ellen L.
CORPORATE SOURCE: Molecular Plant Pathology Laboratory, Plant Sciences Institute, Agricultural Research Service-USDA, Beltsville, MD, 20705, USA
davisr@ba.ars.usda.gov
SOURCE: Microbiological Research, (2003) Vol. 158, No. 3, pp. 229-236. print.
ISSN: 0944-5013.
DOCUMENT TYPE: Article
LANGUAGE: English
OTHER SOURCE: GenBank-AF190224; GenBank-AF190225
ENTRY DATE: Entered STN: 24 Dec 2003
Last Updated on STN: 24 Dec 2003

AB Ribosomal (r) RNA interoperon sequence heterogeneity in the 'Fragaria multicipita' phytoplasma, a member of group 16SrVI, was initially observed in RFLP patterns of rDNA amplified in the polymerase chain reaction (PCR). and was confirmed through sequence analysis of cloned rDNA. Sequences from operons rrnA and rrnB were amplified in PCR primed by primer pair P1/P7 but from only rrnA in PCR primed by primer pair R16mF2/R16mR1. Preferential amplification of DNA from operon rrnA was explained by base mismatches between the R16mF2/R16mR1 primers and primer annealing sites in rrnB. The results revealed potential for classification of a phytoplasma into two different subgroups within a 16S rRNA group, if the phytoplasma's 16S rRNA gene sequences are independently characterized. It is suggested that the rRNA operon containing species-specific signature sequence(s) should be specified, and where possible sequences from both 16S rRNA genes should be included, in descriptions of new 'Candidatus Phytoplasma species'.

L8 ANSWER 17 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2003:455344 BIOSIS
DOCUMENT NUMBER: PREV200300455344
TITLE: Intracellular bacteria associated with the ascidian Ecteinascidia turbinata: Phylogenetic and in situ hybridisation analysis.
AUTHOR(S): Moss, C. [Reprint Author]; Green, D. H.; Perez, B.; Velasco, A.; Henriquez, R.; McKenzie, J. D.
CORPORATE SOURCE: Marine Resource Centre, Integrin Advanced Biosystems, Barcaldine, Oban, Argyll, PA37 1SE, UK
claire_moss@yahoo.com
SOURCE: Marine Biology (Berlin), (July 2003) Vol. 143, No. 1, pp. 99-110. print.
CODEN: MBIOAJ. ISSN: 0025-3162.
DOCUMENT TYPE: Article
LANGUAGE: English

ENTRY DATE: Entered STN: 1 Oct 2003
Last Updated on STN: 1 Oct 2003

AB The ascidian Ecteinascidia turbinata (Herdman) is a colonial sea squirt found in the Caribbean and Mediterranean Seas. In the present study, the bacterial complement of E. turbinata has been assessed by 16S rRNA gene analysis and the most commonly occurring strains identified by restriction fragment length polymorphism. Three strains were found to predominate using this approach, with one representing >50% of clones from both larval and adult material. The 16S rRNA gene sequence of the most commonly occurring strain did not match with any known bacterial sequences and could only be assigned to the gamma-proteobacteria subdivision. The two other frequently occurring strains were assigned to the Mollicutes. In situ hybridisation analysis with eubacterial probes to 16S rRNA revealed the presence of apparently endosymbiotic bacteria in adult and larval tissue, and electron microscopy confirmed the presence of putative bacteriocytes in the larval tissue. The presence of the same bacteria in the brooded larvae suggested that they were vertically transmitted from parent to offspring. Further hybridisation using a novel probe designed to be specific to the 16S rRNA sequence of the dominant strain, highlighted the same cell types as that revealed by the eubacterial probe. The results suggest that the bacteria represent a novel strain, denoted " Candidatus Endoecteinascidia frumentensis", and that they may have an important role in the biology of E. turbinata.

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ACCESSION NUMBER: 2001:778341 SCISEARCH
THE GENUINE ARTICLE: 476PJ
TITLE: Evidence for the biosynthesis of bryostatins by the bacterial symbiont "Candidatus Endobugula sertula" of the bryozoan Bugula neritina
AUTHOR: Davidson S K; Allen S W; Lim G E; Anderson C M; Haygood M G (Reprint)
CORPORATE SOURCE: Univ Calif San Diego, Scripps Inst Oceanog, Div Marine Biol Res, Ctr Marine Biomed & Biotechnol, 0202, La Jolla, CA 92093 USA (Reprint); Univ Calif San Diego, Scripps Inst Oceanog, Div Marine Biol Res, Ctr Marine Biomed & Biotechnol, La Jolla, CA 92093 USA; Univ Calif San Diego, Ctr Canc, La Jolla, CA 92093 USA; CalBioMarine Technol Inc, Carlsbad, CA 92009 USA
COUNTRY OF AUTHOR: USA
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (OCT 2001) Vol. 67, No. 10, pp. 4531-4537.
ISSN: 0099-2240.
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 34
ENTRY DATE: Entered STN: 12 Oct 2001
Last Updated on STN: 12 Oct 2001
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The marine bryozoan, Bugula neritina, is the source of the bryostatins, a family of macrocyclic lactones with anticancer activity. Bryostatins have long been suspected to be bacterial products. B. neritina harbors the uncultivated gamma proteobacterial symbiont "Candidatus Endobugula sertula." In this work several lines of evidence are presented that show that the symbiont is the most likely source of bryostatins. Bryostatins are complex polyketides similar to bacterial secondary metabolites synthesized by modular type I polyketide synthases (PKS-I). PKS-I gene fragments were cloned from DNA extracted from the B. neritina-"E. sertula" association, and then primers specific to one of these clones, KSa, were shown to amplify the KSa gene specifically and universally from total B. neritina DNA. In addition, a

KSa RNA probe was shown to bind specifically to the symbiotic bacteria located in the pallial sinus of the larvae of B. neritina and not to B. neritina cells or to other bacteria. Finally, B. neritina colonies grown in the laboratory were treated with antibiotics to reduce the numbers of bacterial symbionts. Decreased symbiont levels resulted in the reduction of the KSa signal as well as the bryostatin content. These data provide evidence that the symbiont E. sertula has the genetic potential to make bryostatins and is necessary in full complement for the host bryozoan to produce normal levels of bryostatins. This study demonstrates that it may be possible to clone bryostatin genes from B. neritina directly and use these to produce bryostatins in heterologous host bacteria.

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ACCESSION NUMBER: 2001:279067 SCISEARCH
THE GENUINE ARTICLE: 415NY
TITLE: In situ identification of polyphosphate- and polyhydroxyalkanoate-accumulating traits for microbial populations in a biological phosphorus removal process
AUTHOR: Liu W T (Reprint); Nielsen A T; Wu J H; Tsai C S; Matsuo Y; Molin S
CORPORATE SOURCE: Natl Cent Univ, Grad Inst Environm Engn, Chungli 32054, Taiwan (Reprint); Tech Univ Denmark, Dept Microbiol, Mol Microbial Ecol Grp, DK-2800 Lyngby, Denmark; Natl Cheng Kung Univ, Dept Environm Engn, Tainan 70101, Taiwan; Chuo Univ, Dept Civil Engn, Tokyo 112, Japan
COUNTRY OF AUTHOR: Taiwan; Denmark; Japan
SOURCE: ENVIRONMENTAL MICROBIOLOGY, (FEB 2001) Vol. 3, No. 2, pp. 110-122.
ISSN: 1462-2912.
PUBLISHER: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 49
ENTRY DATE: Entered STN: 13 Apr 2001
Last Updated on STN: 13 Apr 2001

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Polyphosphate- and polyhydroxyalkanoate (PHA)- accumulating traits of predominant microorganisms in an efficient enhanced biological phosphorus removal (EBPR) process were investigated systematically using a suite of non-culture-dependent methods. Results of 16S rDNA clone library and fluorescence in situ hybridization (FISH) with rRNA-targeted, group-specific oligonucleotide probes indicated that the microbial community consisted mostly of the alpha- (9.5% of total cells), beta- (41.3%) and gamma- (6.8%) subclasses of the class Proteobacteria, Flexibacter-Cytophaga (4.5%) and the Gram-positive high G+C (HGC) group (17.9%), With individual phylogenetic groups or subgroups, members of Candidatus Accumulibacter phosphatis in the beta -2 subclass, a novel HGC group closely related to Tetrasphaera spp., and a novel gamma -proteobacterial group were the predominant populations. Furthermore, electron microscopy with energy-dispersive X-ray analysis was used to validate the staining specificity of 4,6-diamino-2-phenylindole (DAPI) for intracellular polyphosphate and revealed the composition of polyphosphate granules accumulated in predominant bacteria as mostly P, Ca and Na. As a result, DAPI and PHA staining procedures could be combined with FISH to identify directly the polyphosphate- and PHA-accumulating traits of different phylogenetic groups. Members of Accumulibacter phosphatis and the novel gamma-proteobacterial group were observed to accumulate both polyphosphate and PHA. In addition, one novel rod-shaped group, closely related to coccus-shaped Tetrasphaera, and one filamentous group resembling Candidatus Nostocoidia limicola in the HGC group were found to accumulate polyphosphate but not PHA, No cellular inclusions were detected in most members of the alpha -Proteobacteria and the

Cytophaga-Flavobacterium group. The diversified functional traits observed suggested that different substrate metabolisms were used by predominant phylogenetic groups in EBPR processes.

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ACCESSION NUMBER: 2001:203730 BIOSIS
DOCUMENT NUMBER: PREV200100203730
TITLE: Molecular retrieval of large 16S rRNA gene fragments from an Italian rice paddy soil affiliated with the class Actinobacteria.
AUTHOR(S): Luedemann, Heiner; Conrad, Ralf [Reprint author]
CORPORATE SOURCE: Max-Planck-Institut fuer Terrestrische Mikrobiologie, Karl-von-Frisch-Str., D-35043, Marburg, Germany conrad@mailer.uni-marburg.de
SOURCE: Systematic and Applied Microbiology, (December, 2000) Vol. 23, No. 4, pp. 582-584. print.
CODEN: SAMIDF. ISSN: 0723-2020.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 25 Apr 2001
Last Updated on STN: 18 Feb 2002

AB We designed a PCR assay specific for the 16S rRNA genes of members of the class Actinobacteria, and created a clone library using the amplification product of total community DNA extracted from anoxic Italian rice field soil. Eighteen out of 27 randomly sequenced clones were affiliated with Actinobacteria, i.e. Frankineae, Corynebacterineae, Micrococcineae, the bacterium candidatus "Microthrix parvicella" and a novel taxonomically undefined cluster.

L8 ANSWER 21 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2000:710911 SCISEARCH
THE GENUINE ARTICLE: 352ZQ
TITLE: Search and discovery strategies for biotechnology: The paradigm shift
AUTHOR: Bull A T (Reprint); Ward A C; Goodfellow M
CORPORATE SOURCE: Univ Kent, Res Sch Biosci, Canterbury CT2 7NJ, Kent, England (Reprint); Univ Newcastle, Dept Agr & Environm Sci, Newcastle Upon Tyne NE1 7RU, Tyne & Wear, England
COUNTRY OF AUTHOR: England
SOURCE: MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS, (SEP 2000) Vol. 64, No. 3, pp. 573-+.
ISSN: 1092-2172.
PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 503
ENTRY DATE: Entered STN: 2000
Last Updated on STN: 2000
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Profound changes are occurring in the strategies that biotechnology-based industries are deploying in the search for exploitable biology and to discover new products and develop new or improved processes. The advances that have been made in the past decade in areas such as combinatorial chemistry, combinatorial biosynthesis, metabolic pathway engineering, gene shuffling, and directed evolution of proteins have caused some companies to consider withdrawing from natural product screening. In this review we examine the paradigm shift from traditional biology to bioinformatics that is revolutionizing exploitable biology. We conclude that the reinvigorated means of detecting novel organisms, novel chemical structures, and novel biocatalytic activities will ensure that natural products will continue to be a primary resource for biotechnology.

The paradigm shift has been driven by a convergence of complementary technologies, exemplified by DNA sequencing and amplification genome sequencing and annotation, proteome analysis and phenotypic inventorying, resulting in the establishment of huge databases that can be mined in order to generate useful knowledge such as the identity and characterization of organisms and the identity of biotechnology targets. Concurrently there have been major advances in understanding the extent of microbial diversity, how uncultured organisms might be grown, and how expression of the metabolic potential of microorganisms can be maximized. The integration of information from complementary databases presents a significant challenge. Such integration should facilitate answers to complex questions involving sequence, biochemical, physiological, taxonomic, and ecological information of the sort posed in exploitable biology. The paradigm shift which we discuss is not absolute in the sense that it will replace established microbiology; rather, it reinforces our view that innovative microbiology is essential for releasing the potential of microbial diversity for biotechnology penetration throughout industry Various of these issues are considered with reference to deep-sea microbiology and biotechnology.

L8 ANSWER 22 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2000:865854 SCISEARCH
THE GENUINE ARTICLE: 373DC
TITLE: Phytoplasma: Phytopathogenic mollicutes
AUTHOR: Lee I M (Reprint); Davis R E; Gundersen-Rindal D E
CORPORATE SOURCE: USDA ARS, Mol Plant Pathol Lab, Beltsville, MD 20705 USA (Reprint); USDA ARS, Insect Biocontrol Lab, Beltsville, MD 20705 USA
COUNTRY OF AUTHOR: USA
SOURCE: ANNUAL REVIEW OF MICROBIOLOGY, (2000) Vol. 54, pp. 221-255
ISSN: 0066-4227.
PUBLISHER: ANNUAL REVIEWS, 4139 EL CAMINO WAY, PO BOX 10139, PALO ALTO, CA 94303-0139 USA.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 182
ENTRY DATE: Entered STN: 2000
Last Updated on STN: 2000
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB During the past decade, research has yielded new knowledge about the plant and insect host ranges, geographical distribution, and phylogenetic relationships of phytoplasmas, and a taxonomic system hasemerged in which distinct phytoplasmas are named as separate "Candidatus phytoplasma species." In large part, this progress has resulted from the development and use of molecular methods to detect, identify, and classify phytoplasmas. While these advances continue, research has recently begun on the phytoplasma genome, how phytoplasmas cause disease, the role of mixed phytoplasmal infections in plant diseases, and molecular/genetic phenomena that underlie symptom development in plants. These and other recent advances are laying the foundation for future progress in understanding the mechanisms of phytoplasma pathogenicity, organization of the phytoplasma genome, evolution of new phytoplasma strains and emergence of new diseases, bases of insect transmissibility and specificity of transmission, and plant gene expression in response to phytoplasmal infection, as well as the design of novel approaches to achieve effective control of phytoplasmal diseases.

L8 ANSWER 23 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2000:83089 BIOSIS
DOCUMENT NUMBER: PREV200000083089
TITLE: Enrichment, phylogenetic analysis and detection of a

bacterium that performs enhanced biological phosphate removal in activated sludge.

AUTHOR(S): Hesselmann, Rolf P. X. [Reprint author]; Werlen, Christoph [Reprint author]; Hahn, Dittmar; van der Meer, Jan Roelof [Reprint author]; Zehnder, Alexander J. B. [Reprint author]

CORPORATE SOURCE: Swiss Federal Institute for Environmental Science and Technology (EAWAG) and Swiss Federal Institute of Technology (ETH), Dubendorf, Switzerland

SOURCE: Systematic and Applied Microbiology, (Sept., 1999) Vol. 22, No. 3, pp. 454-465. print.
CODEN: SAMIDF. ISSN: 0723-2020.

DOCUMENT TYPE: Article

LANGUAGE: English

ENTRY DATE: Entered STN: 1 Mar 2000
Last Updated on STN: 3 Jan 2002

AB Activated sludge communities which performed enhanced biological phosphate removal (EBPR) were phylogenetically analyzed by 16S rRNA-targeted molecular methods. Two anaerobic-aerobic sequencing batch reactors were operated with two different carbon sources (acetate vs. a complex mixture) for three years and showed anaerobic-aerobic cycles of polyhydroxybutyrate- (PHB) and phosphate-accumulation characteristic for EBPR-systems. In situ hybridization showed that the reactor fed with the acetate medium was dominated by bacteria phylogenetically related to the Rhodocyclus-group within the beta-Proteobacteria (81% of DAPI-stained cells). The reactor with the complex medium was also predominated by this phylogenetic group albeit at a lesser extent (23% of DAPI-stained cells). More detailed taxonomic information on the dominant bacteria in the acetate-reactor was obtained by constructing clone libraries of 16S rDNA fragments. Two different types of Rhodocyclus-like clones (R1 and R6) were retrieved. Type-specific in situ hybridization and direct rRNA-sequencing revealed that R6 was the type of the dominant bacteria. Staining of intracellular polyphosphate- and PHB-granules confirmed that the R6-type bacterium accumulates PHB and polyphosphate just as predicted by the metabolic models for EBPR. High similarities to 16S rDNA fragments from other EBPR-sludges suggest that R6-type organisms were present and may play an important role in EBPR in general. Although the R6-type bacterium is closely related to the genus Rhodocyclus, it did not grow phototrophically. Therefore, we propose a provisional new genus and species Candidatus Accumulibacter phosphatis.

L8 ANSWER 24 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN DUPLICATE 3

ACCESSION NUMBER: 1998:313109 BIOSIS

DOCUMENT NUMBER: PREV199800313109

TITLE: An approach to characterizing uncultivated prokaryotes: The Grey Lung agent and proposal of a Candidatus taxon for the organism, 'Candidatus Mycoplasma ravipulmonis'.

AUTHOR(S): Neimark, Harold [Reprint author]; Mitchelmore, Deborah; Leach, Ronald H.

CORPORATE SOURCE: Dep. Microbiol. Immunol., Morse Inst. Mol. Biol., State Univ. New York Health Sciences Cent. Brooklyn, Brooklyn, NY 11203, USA

SOURCE: International Journal of Systematic Bacteriology, (April, 1998) Vol. 48, No. 2, pp. 389-394. print.
CODEN: IJSBA8. ISSN: 0020-7713.

DOCUMENT TYPE: Article

LANGUAGE: English

ENTRY DATE: Entered STN: 22 Jul 1998
Last Updated on STN: 22 Jul 1998

AB An approach to characterizing uncultivated bacteria which combines a PFGE procedure for obtaining purified full-length chromosomes with PCR amplification is described. Isolated chromosomes from uncultivated

organisms provide a specifically identifiable source material for hybridization, amplification and cloning. The availability of purified chromosomes for DNA amplification should aid in examining the diversity of microbial populations and should also reduce the possibility of forming hybrid DNA artifact molecules. The approach is illustrated by isolating the chromosome of the uncultivated agent of rodent Grey Lung disease and using the purified chromosomes to amplify and directly sequence the evolutionarily conserved 16S rRNA gene. The Grey Lung agent (GLA) contains a 650 kb chromosome and is shown to be a Mycoplasma sp. located phylogenetically in the hominis group of mycoplasmas. If a simple genomic lesion(s) is responsible for the unculturability of GLA, it is conceivable that complementation with DNA from a close relative could permit growth on artificial media.

L8 ANSWER 25 OF 26 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 1996:533055 BIOSIS
DOCUMENT NUMBER: PREV199699255411
TITLE: Molecular biological evidence for the occurrence of uncultured members of the actinomycete line of descent in different environments and geographical locations.
AUTHOR(S): Rheims, Holger; Sproer, Cathrin; Rainey, Fred A.; Stackebrandt, Erko [Reprint author]
CORPORATE SOURCE: DSMZ-Deutsche Sammlung von Mikroorg. Zellkulturen GmbH, Mascheroder Weg 1b, 38124 Braunschweig, Germany
SOURCE: Microbiology (Reading), (1996) Vol. 142, No. 10, pp. 2863-2870.
ISSN: 1350-0872.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 10 Dec 1996
Last Updated on STN: 10 Dec 1996

AB A 16S rDNA based molecular ecological study was performed on a sample taken from a peat bog in Germany. Total DNA was extracted by directly lysing micro-organisms in the peat matrix. The 5' 1400 nucleotides of the bacterial 16S rDNA were amplified using conserved bacterial PCR primers. A clone library was generated by blunt-end cloning and 262 165 rDNA clones were analysed. Of these, 37 were located in the Gram-positive phylum, as determined by hybridization to an oligonucleotide probe specific for Gram-positive bacteria. Analysis of 17 of these clones by sequence analysis and their comparison with published sequences representing all of the main bacterial phyla indicated their membership of the actinomycete line of descent. These peat clones were found to represent three novel lineages, two of which appear to be related to the species Acidimicrobium ferrooxidans, and 'Candidatus Microthrix parvicella'. Clone sequences of the third group are phylogenetically related to Rubrobacter radiotolerans. Comparison with short 165 rDNA clone sequences obtained from DNA isolated from a geothermally heated soil in New Zealand, and from DNA isolated from soil in Australia, Japan and Finland and marine environments from the Atlantic and the Pacific Oceans, suggests that members of these three groups occur in very different environments across the world.

L8 ANSWER 26 OF 26 SCISEARCH COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 1995:700885 SCISEARCH
THE GENUINE ARTICLE: RZ216
TITLE: COMPARISON OF 16S RIBOSOMAL-RNA SEQUENCES OF SEGMENTED FILAMENTOUS BACTERIA ISOLATED FROM MICE, RATS, AND CHICKENS AND PROPOSAL OF CANDIDATUS ARTHROMITUS
AUTHOR: SNEL J (Reprint); HEINEN P P; BLOK H J; CARMAN R J; DUNCAN A J; ALLEN P C; COLLINS M D
CORPORATE SOURCE: UNIV NIJMEGEN, CENT ANIM LAB, POB 9101, 6500 HB NIJMEGEN,

NETHERLANDS (Reprint); WAGENINGEN UNIV AGR, DEPT MICROBIOL, 6703 CT WAGENINGEN, NETHERLANDS; TECH LAB INC, BLACKSBURG, VA 24060; VIRGINIA POLYTECH INST & STATE UNIV, VIRGINIA MARYLAND REG COLL VET MED, BLACKSBURG, VA 24061; USDA, INST LIVESTOCK & POULTRY SCI, PROTOZOAN DIS LAB, BELTSVILLE, MD 20705; INST FOOD RES, DEPT MICROBIOL, READING RG6 2EF, BERKS, ENGLAND

COUNTRY OF AUTHOR: NETHERLANDS; USA; ENGLAND
SOURCE: INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, (OCT 1995) Vol. 45, No. 4, pp. 780-782.
ISSN: 0020-7713.
PUBLISHER: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 21
ENTRY DATE: Entered STN: 1995
Last Updated on STN: 1995

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Segmented filamentous bacteria (SFB) are nonpathogenic bacteria that are commonly found attached to the intestinal walls of many animals, Until now, these bacteria have not been cultured in vitro, Recently, a 16S rRNA sequence analysis revealed that SFB isolated from mice represent a distinct subline within the Clostridium subphylum of the gram-positive bacteria, Since SFB isolated from mice, rats, and chickens are known to be host specific, we investigated the phylogenetic relationships among SFB obtained from these three hosts, Total DNAs from the intestinal floras of chickens and rats were used as templates for PCR amplification of 16S rRNA genes, BCR products were cloned and screened by a dot blot hybridization procedure to identify homologous sequences that cross-reacted with mouse SFB-specific oligonucleotide probes, A phylogenetic analysis of these 16S ribosomal DNA sequences revealed that SFB isolated from these three hosts form a natural group, which is peripherally related to the genus Clostridium sensu stricto (group I Clostridium), The SFB obtained from chickens, rats, and mice had closely related, albeit different, 16S rRNA gene sequences, The observed levels of 16S rRNA sequence divergence, ca, 1.5 to 3%, together with host specificity, suggest that SFB isolated from mice, rats, and chickens represent different species and that coevolution of the SFB and their hosts occurred, ''Candidatus Arthromitus'' is proposed as the provisional generic name for this group of organisms,

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E1          120     ESTEBAN B/AU
E2           23     ESTEBAN B M/AU
E3            0 --> ESTEBAN B P/AU
E4            3     ESTEBAN BARRAGAN M A/AU
E5            3     ESTEBAN BARRAGAN MIGUEL A/AU
E6            1     ESTEBAN BARRANCO F/AU
E7            1     ESTEBAN BARRIOS B/AU
E8            1     ESTEBAN BELASCO EDUARDO/AU
E9            1     ESTEBAN BENAVIDES B/AU
E10           1     ESTEBAN BERMUDEZ JOSE M/AU
E11           1     ESTEBAN BERNALDEZ J/AU
E12          13     ESTEBAN BERNALDEZ J M/AU

=> e perez t a/au
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E2          621     PEREZ T/AU
E3            4 --> PEREZ T A/AU
E4            1     PEREZ T A T/AU
E5            2     PEREZ T ALDEIMA T/AU
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E11           1      PEREZ T FERNANDEZ/AU
E12          28      PEREZ T H/AU

=> s e2
L9          621 "PEREZ T"/AU

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E3            1 --> IGLESIAS A V/AU
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E5            2      IGLESIAS ADAM/AU
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E7            1      IGLESIAS AGUSTIN/AU
E8            6      IGLESIAS AINHOA/AU
E9            1      IGLESIAS ALAN/AU
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E11         116      IGLESIAS ALBERTO A/AU
E12           4      IGLESIAS ALBERTO ALVARO/AU

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E3            0 --> PELAEZ R H/AU
E4           12      PELAEZ R J/AU
E5            2      PELAEZ R M G/AU
E6            2      PELAEZ R M GIO/AU
E7            8      PELAEZ R MADRONERO/AU
E8            4      PELAEZ R N/AU
E9           38      PELAEZ R P/AU
E10           1      PELAEZ R PALACIOS/AU
E11          35      PELAEZ RAFAEL/AU
E12           1      PELAEZ RAMON MADRO NERO/AU

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E1            1      MORENO R JUAN JOSE/AU
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E3           48 --> MORENO R M/AU
E4           15      MORENO R M B/AU
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E6            1      MORENO R MA/AU
E7            1      MORENO R NORALBA/AU
E8           13      MORENO R O/AU
E9           25      MORENO R P/AU
E10           1      MORENO R PARADA/AU
E11           1      MORENO R PENA/AU
E12           4      MORENO R R/AU

=> s e3-e6
L10          66 ("MORENO R M"/AU OR "MORENO R M B"/AU OR "MORENO R M G"/AU OR
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=> d his

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     LIFESCI' ENTERED AT 16:17:37 ON 19 APR 2007
L1           10 S GAMMA (W) PROTOBACTER?
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L2             0 S CANDIDATUS (W)ENDOECETEIUNASCIDIA
L3          1838 S CANDIDATUS
L4         14868 S 16S (W)RIBOSOMAL(W)RNA
L5           114 S L3 AND L4
L6       8300433 S CLON? OR EXPRESS? OR RECOMBINANT
L7            33 S L5 AND L6
L8            26 DUP REM L7 (7 DUPLICATES REMOVED)
                 E ESTEBAN B P/AU
                 E PEREZ T A/AU
L9           621 S E2
                 E IGLESIAS A V/AU
                 E PELAEZ R H/AU
                 E MORENO R M/AU
L10           66 S E3-E6

=> s l9 or l10
L11          687 L9 OR L10

=> s l5 and l11
L12            0 L5 AND L11

=> d his

     (FILE 'HOME' ENTERED AT 16:17:08 ON 19 APR 2007)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 16:17:37 ON 19 APR 2007
L1            10 S GAMMA (W)PROTOBACTER?
L2             0 S CANDIDATUS (W)ENDOECETEIUNASCIDIA
L3          1838 S CANDIDATUS
L4         14868 S 16S (W)RIBOSOMAL(W)RNA
L5           114 S L3 AND L4
L6       8300433 S CLON? OR EXPRESS? OR RECOMBINANT
L7            33 S L5 AND L6
L8            26 DUP REM L7 (7 DUPLICATES REMOVED)
                 E ESTEBAN B P/AU
                 E PEREZ T A/AU
L9           621 S E2
                 E IGLESIAS A V/AU
                 E PELAEZ R H/AU
                 E MORENO R M/AU
L10           66 S E3-E6
L11          687 S L9 OR L10
L12            0 S L5 AND L11
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	Pages	Document ID	Issue Date	Title
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2	40	US 20040254075 A1	20041216	Chickweed bioherbicides
3	41	US 7141407 B2	20061128	Chickweed bioherbicides
4	20	US 6664081 B2	20031216	Nucleic acid amplification and detection of mycobacterium species
5	49	US 6287828 B1	20010911	Method for producing amide compounds using a nitrile hydratase from a thermophilic bacillus
6	49	US 6242242 B1	20010605	Method for producing amide compounds using a nitrile hydratase from a thermophilic bacillus
7	48	US 6228633 B1	20010508	Method for producing amide compounds using a nitrile hydratase from a thermophilic bacillus
8	48	US 6214603 B1	20010410	Method for producing amide compounds using a nitrile hydratase from a thermophilic bacillus
9	49	US 6153415 A	20001128	Method for producing amide compounds using a nitrile hydratase from a thermophilic bacillus

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1	L1	39	candidatus
2	L2	9	16S adj ribosomal adj rRNA
3	L3	0	l1 same l2
4	L4	958318	clon$3 or express$3 or recombinant
5	L5	0	l2 same l4
6	L6	15709	PEREZ IGLESIAS PELAEZ MORENO
7	L7	0	l2 and l6
8	L8	157	endosymbiotic
9	L9	9	l6 and l8

US 107068520NP1

Creation date: 04-25-2007
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Dossier: 10706852

Legal Date: 04-23-2007

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3	892	2
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5	NPL	11
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8	NPL	5
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10	NPL	9
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